SEQUENCE LISTING

<110> YAMAMOTO, Hiroshi
TSUJIKAWA, Kazutake
UCHINO, Yukiko

<120> ANTIBODIES SPECIFIC FOR INTRACELLULAR DOMAIN OF PROTEIN TYROSINE PHOSPHATASE

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atc ccc atc acc gac ctg gcg gac aac atc gag cgc ctc aaa gcc aac   146
Ile Pro Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg Leu Lys Ala Asn
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Gln Phe Thr Trp Glu Asn Ser Asn Leu Glu Val Asn Lys Pro Lys Asn
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cgc tat gcg aat gtc atc gcc tac gac cac tct cga gtc atc ctt acc   290
Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val Ile Leu Thr
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tct atc gat ggc gtc ccc ggg agt gac tac atc aat gcc aac tac atc   338
Ser Ile Asp Gly Val Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile
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gat ggc tac cgc aag cag aat gcc tac atc gcc acg cag ggc ccc ctg   386
Asp Gly Tyr Arg Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu
            115                 120                 125

ccc gag acc atg ggc gat ttc tgg aga atg gtg tgg gaa cag cgc acg   434
Pro Glu Thr Met Gly Asp Phe Trp Arg Met Val Trp Glu Gln Arg Thr
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gcc act gtg gtc atg atg aca cgg ctg gag gag aag tcc cgg gta aaa   482
Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys Ser Arg Val Lys
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Cys Asp Gln Tyr Trp Pro Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile
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cag gtg acc ctg ttg gac aca gtg gag ctg gcc aca tac act gtg cgc   578
Gln Val Thr Leu Leu Asp Thr Val Glu Leu Ala Thr Tyr Thr Val Arg
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acc ttc gca ctc cac aag agt ggc tcc agt gag aag cgt gag ctg cgt   626
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His Thr Ser Arg Phe Ile Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys
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ctg gca gag agc acc gag gac ttc tgg cgc atg cta tgg gag cac aat  1298
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aaa tgc cac cag tac tgg cca gca gag cgc tct gct cgc tac cag tac  1394
Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr
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Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu
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cgg cag ttc cag ttc aca gac tgg cca gag cag ggc gtg ccc aag aca  1538
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ttgtcctggg ctgtggctgg ctgtggagct agagccctgg atggcccctg agccagcccc 360

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Ala Thr Gly Glu Pro Lys Pro Arg Ile Thr Trp Met Lys Lys Gly Lys
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50 55 60

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Gly Ser Val Leu Arg Ile Gln Pro Leu Arg Val Gln Arg Asp Glu Ala
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Ile Tyr Glu Cys Thr Ala Thr Asn Ser Leu Gly Glu Ile Asn Thr Ser
80 85 90

gcc aag ctc tca gtg ctc gaa gag gaa cag ctg ccc cct ggg ttc cct 745
Ala Lys Leu Ser Val Leu Glu Glu Glu Gln Leu Pro Pro Gly Phe Pro
95 100 105

tcc atc gac atg ggg cct cag ctg aag gtg gtg gag aag gca cgc aca 793
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Ile Lys Gln Leu Arg Ser Gly Ala Leu Gln Ile Glu Ser Ser Glu Glu
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    175                 180                 185

cgt tac tca gcc cct gcg aac ctg tat gtg cga gtg cgc cgc gtg gct  1033
Arg Tyr Ser Ala Pro Ala Asn Leu Tyr Val Arg Val Arg Arg Val Ala
190                 195                 200                 205

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Pro Arg Phe Ser Ile Pro Pro Ser Ser Gln Glu Val Met Pro Gly Gly
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agc gtg aac ctg aca tgc gtg gca gtg ggt gca ccc atg ccc tac gtg  1129
Ser Val Asn Leu Thr Cys Val Ala Val Gly Ala Pro Met Pro Tyr Val
            225                 230                 235

aag tgg atg atg ggg gcc gag gag ctc acc aag gag gat gag atg cca  1177
Lys Trp Met Met Gly Ala Glu Glu Leu Thr Lys Glu Asp Glu Met Pro
        240                 245                 250

gtt ggc cgc aac gtc ctg gag ctc agc aat gtc gta cgc tct gcc aac  1225
Val Gly Arg Asn Val Leu Glu Leu Ser Asn Val Val Arg Ser Ala Asn
    255                 260                 265

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Tyr Thr Cys Val Ala Ile Ser Ser Leu Gly Met Ile Glu Ala Thr Ala
270                 275                 280                 285

cag gtc aca gtg aaa gct ctt cca aag cct ccg att gat ctt gtg gtg  1321
Gln Val Thr Val Lys Ala Leu Pro Lys Pro Pro Ile Asp Leu Val Val
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            305                 310                 315

tcg gag cct gta acc tac tat ggc atc cag tac cgc gca gcg ggc acg  1417
Ser Glu Pro Val Thr Tyr Tyr Gly Ile Gln Tyr Arg Ala Ala Gly Thr
        320                 325                 330

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Glu Gly Pro Phe Gln Glu Val Asp Gly Val Ala Thr Thr Arg Tyr Ser
    335                 340                 345

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Ile Gly Gly Leu Ser Pro Phe Ser Glu Tyr Ala Phe Arg Val Leu Ala
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Thr Gly Glu Gln Ala Pro Ser Ser Pro Pro Arg Arg Val Gln Ala Arg
            385                 390                 395

atg ctg agc gcc agc acc atg ctg gtg cag tgg gag cct ccc gag gag   1657
Met Leu Ser Ala Ser Thr Met Leu Val Gln Trp Glu Pro Pro Glu Glu
        400                 405                 410

ccc aac ggc ctg gtg cgg gga tac cgc gtc tac tat act ccg gac tcc   1705
Pro Asn Gly Leu Val Arg Gly Tyr Arg Val Tyr Tyr Thr Pro Asp Ser
    415                 420                 425

cgc cgc ccc ccg aac gcc tgg cac aag cac aac acc gac gcg ggg ctc   1753
Arg Arg Pro Pro Asn Ala Trp His Lys His Asn Thr Asp Ala Gly Leu
430                 435                 440                 445

ctc acg acc gtg ggc agc ctg ctg cct ggc atc acc tac agc ctg cgc   1801
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                450                 455                 460

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Val Leu Ala Phe Thr Ala Val Gly Asp Gly Pro Pro Ser Pro Thr Ile
            465                 470                 475

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Gln Val Lys Thr Gln Gln Gly Val Pro Ala Gln Pro Ala Asp Phe Gln
        480                 485                 490

gcc gag gtg gag tcg gac acc agg atc cag ctc tcg tgg ctg ctg ccc   1945
Ala Glu Val Glu Ser Asp Thr Arg Ile Gln Leu Ser Trp Leu Leu Pro
    495                 500                 505

cct cag gag cgg atc atc atg tat gaa ctg gtg tac tgg gcg gca gag   1993
Pro Gln Glu Arg Ile Ile Met Tyr Glu Leu Val Tyr Trp Ala Ala Glu
510                 515                 520                 525

gac gaa gac caa cag cac aag gtc acc ttc gac cca acc tcc tcc tac   2041
Asp Glu Asp Gln Gln His Lys Val Thr Phe Asp Pro Thr Ser Ser Tyr
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        560                 565                 570

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Arg Thr Ala Gln Ser Thr Pro Ser Ala Pro Pro Gln Lys Val Met Cys
    575                 580                 585

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Val Ser Met Gly Ser Thr Thr Val Arg Val Ser Trp Val Pro Pro Pro
590                 595                 600                 605

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Arg Glu His Ser Ser Trp Asp Leu Val Gly Leu Glu Lys Trp Thr Glu
        640                 645                 650

tac cgg gtg tgg gtg cgg gca cac aca gac gtg ggc ccc ggc ccc gag   2425
Tyr Arg Val Trp Val Arg Ala His Thr Asp Val Gly Pro Gly Pro Glu
    655                 660                 665

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670                 675                 680                 685

ccg cgg aag gtg gag gtg gag cca ctg aac tcc act gct gtg cat gtc   2521
Pro Arg Lys Val Glu Val Glu Pro Leu Asn Ser Thr Ala Val His Val
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Lys Asp Asp Gln His Phe Thr Val Thr Gly Leu His Lys Gly Thr Thr
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E

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tgg gac ccg cca gtg ctg gcg gag agg aac ggg cgc atc atc agc tac   3193
Trp Asp Pro Pro Val Leu Ala Glu Arg Asn Gly Arg Ile Ile Ser Tyr
910                 915                 920                 925

acc gtg gtg ttc cga gac atc aac agc caa cag gag ctg cag aac atc   3241
Thr Val Val Phe Arg Asp Ile Asn Ser Gln Gln Glu Leu Gln Asn Ile
                930                 935                 940

acg aca gac acc cgc ttt acc ctt act ggc ctc aag cca gac acc act   3289
Thr Thr Asp Thr Arg Phe Thr Leu Thr Gly Leu Lys Pro Asp Thr Thr
            945                 950                 955

tac gac atc aag gtc cgc gca tgg acc agc aaa ggc tct ggc cca ctc   3337
Tyr Asp Ile Lys Val Arg Ala Trp Thr Ser Lys Gly Ser Gly Pro Leu
        960                 965                 970

agc ccc agc atc cag tcc cgg acc atg ccg gtg gag caa gtg ttt gcc   3385
Ser Pro Ser Ile Gln Ser Arg Thr Met Pro Val Glu Gln Val Phe Ala
    975                 980                 985

aag aac ttc cgg gtg gcg gct gca atg aag acg tct gtg ctg ctc agc   3433
Lys Asn Phe Arg Val Ala Ala Ala Met Lys Thr Ser Val Leu Leu Ser
990                 995                1000                1005

tgg gag gtt ccc gac tcc tat aag tca gct gtg ccc ttt aag att ctg   3481
Trp Glu Val Pro Asp Ser Tyr Lys Ser Ala Val Pro Phe Lys Ile Leu
                1010                1015                1020

tac aat ggg cag agt gtg gag gtg gac ggg cac tcg atg cgg aag ctg   3529
Tyr Asn Gly Gln Ser Val Glu Val Asp Gly His Ser Met Arg Lys Leu
            1025                1030                1035

atc gca gac ctg cag ccc aac aca gag tac tcg ttt gtg ctg atg aac   3577
Ile Ala Asp Leu Gln Pro Asn Thr Glu Tyr Ser Phe Val Leu Met Asn
        1040                1045                1050

cgt ggc agc agc gca ggg ggc ctg cag cac ctg gtg tcc atc cgc aca   3625
Arg Gly Ser Ser Ala Gly Gly Leu Gln His Leu Val Ser Ile Arg Thr
    1055                1060                1065

gcc ccc gac ctc ctg cct cac aag ccg ctg cct gcc tct gcc tac ata   3673
Ala Pro Asp Leu Leu Pro His Lys Pro Leu Pro Ala Ser Ala Tyr Ile
1070                1075                1080                1085

gag gac ggc cgc ttc gat ctc tcc atg ccc cat gtg caa gac ccc tcg   3721
Glu Asp Gly Arg Phe Asp Leu Ser Met Pro His Val Gln Asp Pro Ser
                1090                1095                1100

ctt gtc agg tgg ttc tac att gtt gtg gta ccc att gac cgt gtg ggc   3769
Leu Val Arg Trp Phe Tyr Ile Val Val Val Pro Ile Asp Arg Val Gly
            1105                1110                1115

ggg agc atg ctg acg cca agg tgg agc aca ccc gag gaa ctg gag ctg   3817
Gly Ser Met Leu Thr Pro Arg Trp Ser Thr Pro Glu Glu Leu Glu Leu
        1120                1125                1130
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gac gag ctt cta gaa gcc atc gag caa ggc gga gag gag cag cgg cgg   3865
Asp Glu Leu Leu Glu Ala Ile Glu Gln Gly Gly Glu Glu Gln Arg Arg
   1135                1140                1145

cgg cgg cgg cag gca gaa cgt ctg aag cca tat gtg gct gct caa ctg   3913
Arg Arg Arg Gln Ala Glu Arg Leu Lys Pro Tyr Val Ala Ala Gln Leu
1150                1155                1160                1165

gat gtg ctc ccg gag acc ttt acc ttg ggg gac aag aag aac tac cgg   3961
Asp Val Leu Pro Glu Thr Phe Thr Leu Gly Asp Lys Lys Asn Tyr Arg
                1170                1175                1180

ggc ttc tac aac cgg ccc ctg tct ccg gac ttg agc tac cag tgc ttt   4009
Gly Phe Tyr Asn Arg Pro Leu Ser Pro Asp Leu Ser Tyr Gln Cys Phe
            1185                1190                1195

gtg ctt gcc tcc ttg aag gaa ccc atg gac cag aag cgc tat gcc tcc   4057
Val Leu Ala Ser Leu Lys Glu Pro Met Asp Gln Lys Arg Tyr Ala Ser
        1200                1205                1210

agc ccc tac tcg gat gag atc gtg gtc cag gtg aca cca gcc cag cag   4105
Ser Pro Tyr Ser Asp Glu Ile Val Val Gln Val Thr Pro Ala Gln Gln
    1215                1220                1225

cag gag gag ccg gag atg ctg tgg gtg acg ggt ccc gtg ctg gca gtc   4153
Gln Glu Glu Pro Glu Met Leu Trp Val Thr Gly Pro Val Leu Ala Val
1230                1235                1240                1245

atc ctc atc atc ctc att gtc atc gcc atc ctc ttg ttc aaa agg aaa   4201
Ile Leu Ile Ile Leu Ile Val Ile Ala Ile Leu Leu Phe Lys Arg Lys
                1250                1255                1260

agg acc cac tct ccg tcc tct aag gat gag cag tcg atc gga ctg aag   4249
Arg Thr His Ser Pro Ser Ser Lys Asp Glu Gln Ser Ile Gly Leu Lys
            1265                1270                1275

gac tcc ttg ctg gcc cac tcc tct gac cct gtg gag atg cgg agg ctc   4297
Asp Ser Leu Leu Ala His Ser Ser Asp Pro Val Glu Met Arg Arg Leu
        1280                1285                1290

aac tac cag acc cca ggt atg cga gac cac cca ccc atc ccc atc acc   4345
Asn Tyr Gln Thr Pro Gly Met Arg Asp His Pro Pro Ile Pro Ile Thr
    1295                1300                1305

gac ctg gcg gac aac atc gag cgc ctc aaa gcc aac gat ggc ctc aag   4393
Asp Leu Ala Asp Asn Ile Glu Arg Leu Lys Ala Asn Asp Gly Leu Lys
1310                1315                1320                1325

ttc tcc cag gag tat gag tcc atc gac cct gga cag cag ttc acg tgg   4441
Phe Ser Gln Glu Tyr Glu Ser Ile Asp Pro Gly Gln Gln Phe Thr Trp
                1330                1335                1340

gag aat tca aac ctg gag gtg aac aag ccc aag aac cgc tat gcg aat   4489
Glu Asn Ser Asn Leu Glu Val Asn Lys Pro Lys Asn Arg Tyr Ala Asn
            1345                1350                1355

gtc atc gcc tac gac cac tct cga gtc atc ctt acc tct atc gat ggc   4537
Val Ile Ala Tyr Asp His Ser Arg Val Ile Leu Thr Ser Ile Asp Gly
        1360                1365                1370

gtc ccc ggg agt gac tac atc aat gcc aac tac atc gat ggc tac cgc   4585
Val Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Asp Gly Tyr Arg
    1375                1380                1385
```

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aag cag aat gcc tac atc gcc acg cag ggc ccc ctg ccc gag acc atg   4633
Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Met
1390              1395                1400                1405

ggc gat ttc tgg aga atg gtg tgg gaa cag cgc acg gcc act gtg gtc   4681
Gly Asp Phe Trp Arg Met Val Trp Glu Gln Arg Thr Ala Thr Val Val
                  1410                1415                1420

atg atg aca cgg ctg gag gag aag tcc cgg gta aaa tgt gat cag tac   4729
Met Met Thr Arg Leu Glu Glu Lys Ser Arg Val Lys Cys Asp Gln Tyr
            1425                1430                1435

tgg cca gcc cgt ggc acc gag acc tgt ggc ctt att cag gtg acc ctg   4777
Trp Pro Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile Gln Val Thr Leu
        1440                1445                1450

ttg gac aca gtg gag ctg gcc aca tac act gtg cgc acc ttc gca ctc   4825
Leu Asp Thr Val Glu Leu Ala Thr Tyr Thr Val Arg Thr Phe Ala Leu
    1455                1460                1465

cac aag agt ggc tcc agt gag aag cgt gag ctg cgt cag ttt cag ttc   4873
His Lys Ser Gly Ser Ser Glu Lys Arg Glu Leu Arg Gln Phe Gln Phe
1470                1475                1480                1485

atg gcc tgg cca gac cat gga gtt cct gag tac cca act ccc atc ctg   4921
Met Ala Trp Pro Asp His Gly Val Pro Glu Tyr Pro Thr Pro Ile Leu
                  1490                1495                1500

gcc ttc cta cga cgg gtc aag gcc tgc aac ccc cta gac gca ggg ccc   4969
Ala Phe Leu Arg Arg Val Lys Ala Cys Asn Pro Leu Asp Ala Gly Pro
            1505                1510                1515

atg gtg gtg cac tgc agc gcg ggc gtg ggc cgc acc ggc tgc ttc atc   5017
Met Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Cys Phe Ile
        1520                1525                1530

gtg att gat gcc atg ttg gag cgg atg aag cac gag aag acg gtg gac   5065
Val Ile Asp Ala Met Leu Glu Arg Met Lys His Glu Lys Thr Val Asp
    1535                1540                1545

atc tat ggc cac gtg acc tgc atg cga tca cag agg aac tac atg gtg   5113
Ile Tyr Gly His Val Thr Cys Met Arg Ser Gln Arg Asn Tyr Met Val
1550                1555                1560                1565

cag acg gag gac cag tac gtg ttc atc cat gag gcg ctg ctg gag gct   5161
Gln Thr Glu Asp Gln Tyr Val Phe Ile His Glu Ala Leu Leu Glu Ala
                  1570                1575                1580

gcc acg tgc ggc cac aca gag gtg cct gcc cgc aac ctg tat gcc cac   5209
Ala Thr Cys Gly His Thr Glu Val Pro Ala Arg Asn Leu Tyr Ala His
            1585                1590                1595

atc cag aag ctg ggc caa gtg cct cca ggg gag agt gtg acc gcc atg   5257
Ile Gln Lys Leu Gly Gln Val Pro Pro Gly Glu Ser Val Thr Ala Met
        1600                1605                1610

gag ctc gag ttc aag ttg ctg gcc agc tcc aag gcc cac acg tcc cgc   5305
Glu Leu Glu Phe Lys Leu Leu Ala Ser Ser Lys Ala His Thr Ser Arg
    1615                1620                1625

ttc atc agc gcc aac ctg ccc tgc aac aag ttc aag aac cgg ctg gtg   5353
Phe Ile Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys Asn Arg Leu Val
1630                1635                1640                1645
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aac atc atg ccc tac gaa ttg acc cgt gtg tgt ctg cag ccc atc cgt   5401
Asn Ile Met Pro Tyr Glu Leu Thr Arg Val Cys Leu Gln Pro Ile Arg
                1650                1655                1660

ggt gtg gag ggc tct gac tac atc aat gcc agc ttc ctg gat ggt tat   5449
Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe Leu Asp Gly Tyr
            1665                1670                1675

aga cag cag aag gcc tac ata gct aca cag ggg cct ctg gca gag agc   5497
Arg Gln Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ala Glu Ser
        1680                1685                1690

acc gag gac ttc tgg cgc atg cta tgg gag cac aat tcc acc atc atc   5545
Thr Glu Asp Phe Trp Arg Met Leu Trp Glu His Asn Ser Thr Ile Ile
    1695                1700                1705

gtc atg ctg acc aag ctt cgg gag atg ggc agg gag aaa tgc cac cag   5593
Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg Glu Lys Cys His Gln
1710                1715                1720                1725

tac tgg cca gca gag cgc tct gct cgc tac cag tac ttt gtt gtt gac   5641
Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr Phe Val Val Asp
                1730                1735                1740

ccg atg gct gag tac aac atg ccc cag tat atc ctg cgt gag ttc aag   5689
Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu Arg Glu Phe Lys
            1745                1750                1755

gtc acg gat gcc cgg gat ggg cag tca agg aca atc cgg cag ttc cag   5737
Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr Ile Arg Gln Phe Gln
        1760                1765                1770

ttc aca gac tgg cca gag cag ggc gtg ccc aag aca ggc gag gga ttc   5785
Phe Thr Asp Trp Pro Glu Gln Gly Val Pro Lys Thr Gly Glu Gly Phe
    1775                1780                1785

att gac ttc atc ggg cag gtg cat aag acc aag gag cag ttt gga cag   5833
Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu Gln Phe Gly Gln
1790                1795                1800                1805

gat ggg cct atc acg gtg cac tgc agt gct ggc gtg ggc cgc acc ggg   5881
Asp Gly Pro Ile Thr Val His Cys Ser Ala Gly Val Gly Arg Thr Gly
                1810                1815                1820

gtg ttc atc act ctg agc atc gtc ctg gag cgc atg cgc tat gag ggc   5929
Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg Met Arg Tyr Glu Gly
            1825                1830                1835

gtg gtc gac atg ttt cag acc gtg aag acc ctg cgt aca cag cgt cct   5977
Val Val Asp Met Phe Gln Thr Val Lys Thr Leu Arg Thr Gln Arg Pro
        1840                1845                1850

gcc atg gtg cag aca gag gac cag tat cag ctg tgc tac cgt gcg gcc   6025
Ala Met Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys Tyr Arg Ala Ala
    1855                1860                1865

ctg gag tac ctc ggc agc ttt gac cac tat gca acg taactaccgc        6071
Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr
1870                1875                1880

tcccctctcc tccgccaccc ccgccgtggg gctccggagg ggacccagct cctctgagcc 6131

ataccgacca tcgtccagcc ctcctacgca gatgctgtca ctggcagagc acagcccacg 6191
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gggatcacag cgtttcagga acgttgccac accaatcaga gagcctagaa catccctggg 6251

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tcatttttac cttgtggatg ctagtgctgt agagttcact gttgtacaca gtctgttttc 7631

tatttgttaa gaaaaactac agcatcattg cataattctt gatggtaata aatttgaata 7691

atcagatttc t 7702

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<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: Identical
Sequence in Phosphatase Domain 1 of LAR and CD45

<400> 4

Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly
1 5 10

<210> 5
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Unknown Organism: Consensus Amino Acid Sequence in Cytoplasmic Domain of Known PTPs.

<220>
<221> SITE
<222> (3)
<223> Xaa= Arg, Glu or Leu

<220>
<221> SITE
<222> (5)
<223> Xaa= Val, Ile or Cys

<400> 5
Phe Trp Xaa Met Xaa Trp
1 5

<210> 6
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Unknown Organism: Consensus Amino Acid Sequence in Cytoplasmic Domain of Known PTPs.

<220>
<221> SITE
<222> (3)
<223> Xaa= Ala or Asp

<220>
<221> SITE
<222> (4)
<223> Xaa= Gln, Glu or Lys

<400> 6
Lys Cys Xaa Xaa Tyr Trp Pro
1 5

<210> 7
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Unknown Organism: Consensus Amino Acid Sequence in Cytoplasmic Domain of Known PTPs.

<220>
<221> SITE

<222> (4)
<223> Xaa= His or Phe

<400> 7
Trp Pro Asp Xaa Gly Val
1 5

<210> 8
<211> 14
<212> PRT
<213> Artificial sequence

<220>
<223> Description of Unknown Organism: Consensus Amino Acid Sequence in Cytoplasmic Domain of Known PTPs.

<220>
<221> SITE
<222> (2)
<223> Xaa= Unkown

<220>
<221> SITE
<222> (3)
<223> Xaa= Ile or Val

<220>
<221> SITE
<222> (4)
<223> Xaa= Ile or Val

<220>
<221> SITE
<222> (7)
<223> Xaa= Unkown

<220>
<221> SITE
<222> (10)
<223> Xaa= Unknown

<220>
<221> SITE
<222> (13)
<223> Xaa= Thr or Ser

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Pro Xaa Xaa Xaa His Cys Xaa Ala Gly Xaa Gly Arg Xaa Gly
1 5 10

<210> 9
<211> 538
<212> PRT
<213> Homo sapiens

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1 5 10 15

Ala Tyr Asp His Ser Arg Val Ile Leu Thr Ser Ile Asp Gly Val Pro
20 25 30

Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile Asp Gly Tyr Arg Lys Gln
35 40 45

Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Met Gly Asp
50 55 60

Phe Trp Arg Met Val Trp Glu Gln Arg Thr Ala Thr Val Val Met Met
65 70 75 80

Thr Arg Leu Glu Glu Lys Ser Arg Val Lys Cys Asp Gln Tyr Trp Pro
85 90 95

Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile Gln Val Thr Leu Leu Asp
100 105 110

Thr Val Glu Leu Ala Thr Tyr Thr Val Arg Thr Phe Ala Leu His Lys
115 120 125

Ser Gly Ser Ser Glu Lys Arg Glu Leu Arg Gln Phe Gln Phe Met Ala
130 135 140

Trp Pro Asp His Gly Val Pro Glu Tyr Pro Thr Pro Ile Leu Ala Phe
145 150 155 160

Leu Arg Arg Val Lys Ala Cys Asn Pro Leu Asp Ala Gly Pro Met Val
165 170 175

Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Cys Phe Ile Val Ile
180 185 190

Asp Ala Met Leu Glu Arg Met Lys His Glu Lys Thr Val Asp Ile Tyr
195 200 205

Gly His Val Thr Cys Met Arg Ser Gln Arg Asn Tyr Met Val Gln Thr
210 215 220

Glu Asp Gln Tyr Val Phe Ile His Glu Ala Leu Leu Glu Ala Ala Thr
225 230 235 240

Cys Gly His Thr Glu Val Pro Ala Arg Asn Leu Tyr Ala His Ile Gln
245 250 255

Lys Leu Gly Gln Val Pro Pro Gly Glu Ser Val Thr Ala Met Glu Leu
260 265 270

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Glu Phe Lys Leu Leu Ala Ser Ser Lys Ala His Thr Ser Arg Phe Ile
275 280 285

Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys Asn Arg Leu Val Asn Ile
290 295 300

Met Pro Tyr Glu Leu Thr Arg Val Cys Leu Gln Pro Ile Arg Gly Val
305 310 315 320

Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe Leu Asp Gly Tyr Arg Gln
325 330 335

Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ala Glu Ser Thr Glu
340 345 350

Asp Phe Trp Arg Met Leu Trp Glu His Asn Ser Thr Ile Ile Val Met
355 360 365

Leu Thr Lys Leu Arg Glu Met Gly Arg Glu Lys Cys His Gln Tyr Trp
370 375 380

Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr Phe Val Val Asp Pro Met
385 390 395 400

Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu Arg Glu Phe Lys Val Thr
405 410 415

Asp Ala Arg Asp Gly Gln Ser Arg Thr Ile Arg Gln Phe Gln Phe Thr
420 425 430

Asp Trp Pro Glu Gln Gly Val Pro Lys Thr Gly Glu Gly Phe Ile Asp
435 440 445

Phe Ile Gly Gln Val His Lys Thr Lys Glu Gln Phe Gly Gln Asp Gly
450 455 460

Pro Ile Thr Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val Phe
465 470 475 480

Ile Thr Leu Ser Ile Val Leu Glu Arg Met Arg Tyr Glu Gly Val Val
485 490 495

Asp Met Phe Gln Thr Val Lys Thr Leu Arg Thr Gln Arg Pro Ala Met
500 505 510

Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys Tyr Arg Ala Ala Leu Glu
515 520 525

Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr
530 535

<210> 10
<211> 635
<212> PRT
<213> Homo sapiens

<400> 10

Ala Arg Lys Pro Phe Asn Gln Asn Lys Asn Arg Tyr Val Asp Ile Leu
1 5 10 15

Pro Tyr Asp Tyr Asn Arg Val Glu Leu Ser Glu Ile Asn Gly Asp Ala
20 25 30

Gly Ser Asn Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Phe Lys Glu Pro
35 40 45

Arg Lys Tyr Ile Ala Ala Gln Gly Pro Arg Asp Glu Thr Val Asp Asp
50 55 60

Phe Trp Arg Met Ile Trp Glu Gln Lys Ala Thr Val Ile Val Met Val
65 70 75 80

Thr Arg Cys Glu Glu Gly Asn Arg Asn Lys Cys Ala Glu Tyr Trp Pro
85 90 95

Ser Met Glu Glu Gly Thr Arg Ala Phe Gly Asp Val Val Val Lys Ile
100 105 110

Asn Gln His Lys Arg Cys Pro Asp Tyr Ile Ile Gln Lys Leu Asn Ile
115 120 125

Val Asn Lys Lys Glu Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln
130 135 140

Phe Thr Ser Trp Pro Asp His Gly Val Pro Glu Asp Pro His Leu Leu
145 150 155 160

Leu Lys Leu Arg Arg Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly
165 170 175

Pro Ile Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr
180 185 190

Ile Gly Ile Asp Ala Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val
195 200 205

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Asp Val Tyr Gly Tyr Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met
    210                 215                 220

Val Gln Val Glu Ala Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu
225                 230                 235                 240

Tyr Asn Gln Phe Gly Glu Thr Glu Val Asn Leu Ser Glu Leu His Pro
                245                 250                 255

Tyr Leu His Asn Met Lys Lys Arg Asp Pro Pro Ser Glu Pro Ser Pro
            260                 265                 270

Leu Glu Ala Glu Phe Gln Arg Leu Pro Ser Tyr Arg Ser Trp Arg Thr
        275                 280                 285

Gln His Ile Gly Asn Gln Glu Glu Asn Lys Ser Lys Asn Arg Asn Ser
    290                 295                 300

Asn Val Ile Pro Tyr Asp Tyr Asn Arg Val Pro Leu Lys His Glu Leu
305                 310                 315                 320

Glu Met Ser Lys Glu Ser Glu His Asp Ser Asp Glu Ser Ser Asp Asp
                325                 330                 335

Asp Ser Asp Ser Glu Glu Pro Ser Lys Tyr Ile Asn Ala Ser Phe Ile
            340                 345                 350

Met Ser Tyr Trp Lys Pro Glu Val Met Ile Ala Ala Gln Gly Pro Leu
        355                 360                 365

Lys Glu Thr Ile Gly Asp Phe Trp Gln Met Ile Phe Gln Arg Lys Val
    370                 375                 380

Lys Val Ile Val Met Leu Thr Glu Leu Lys His Gly Asp Gln Glu Ile
385                 390                 395                 400

Cys Ala Gln Tyr Trp Gly Glu Gly Lys Gln Thr Tyr Gly Asp Ile Glu
                405                 410                 415

Val Asp Leu Lys Asp Thr Asp Lys Ser Ser Thr Tyr Thr Leu Arg Val
            420                 425                 430

Phe Glu Leu Arg His Ser Lys Arg Lys Asp Ser Arg Thr Val Tyr Gln
        435                 440                 445

Tyr Gln Tyr Thr Asn Trp Ser Val Glu Gln Leu Pro Ala Glu Pro Lys
    450                 455                 460
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Glu Leu Ile Ser Met Ile Gln Val Val Lys Gln Lys Leu Pro Gln Lys
465                 470                 475                 480

Asn Ser Ser Glu Gly Asn Lys His His Lys Ser Thr Pro Leu Leu Ile
                485                 490                 495

His Cys Arg Asp Gly Ser Gln Gln Thr Gly Ile Phe Cys Ala Leu Leu
            500                 505                 510

Asn Leu Leu Glu Ser Ala Glu Thr Glu Glu Val Val Asp Ile Phe Gln
        515                 520                 525

Val Val Lys Ala Leu Arg Lys Ala Arg Pro Gly Met Val Ser Thr Phe
    530                 535                 540

Glu Gln Tyr Gln Phe Leu Tyr Asp Val Ile Ala Ser Thr Tyr Pro Ala
545                 550                 555                 560

Gln Asn Gly Gln Val Lys Lys Asn Asn His Gln Glu Asp Lys Ile Glu
                565                 570                 575

Phe Asp Asn Glu Val Asp Lys Val Lys Gln Asp Ala Asn Cys Val Asn
            580                 585                 590

Pro Leu Gly Ala Pro Glu Lys Leu Pro Glu Ala Lys Glu Gln Ala Glu
        595                 600                 605

Gly Ser Glu Pro Thr Ser Gly Thr Glu Gly Pro Glu His Ser Val Asn
    610                 615                 620

Gly Pro Ala Ser Pro Ala Leu Asn Gln Gly Ser
625                 630                 635
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August 27, 2003

FACSIMILE TRANSMISSION SHEET

TO	Examiner Maher M. Haddad -- Group 1644
COMPANY	U.S. Patent and Trademark Office
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FROM: Kurt T. Buechle
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MESSAGE:

RE: APPLICATION NO. 09/743,492

Please contact Carol Michalec at (312) 474-9526 if you do not receive all of the pages in good condition.

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PATENT
19036/37023

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Yamamoto, *et al.*

Serial No: 09/743,492

Filed: April 30, 2001

Title: Antibodies Specific for Intracellular Domain of Protein Tyrosine Phosphatase

Group Art Unit: 1642

Examiner: M. M. Haddad

VIA HAND DELIVERY

STATEMENT UNDER 37 C.F.R. §§1.825(a) and (b)

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

Sir:

I hereby state that the content of the paper and computer readable copies of the substitute Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same and include no new matter. Sequences 1-8 find support in the sequence listing as originally filed; sequences 9 and 10 find support in Figure 9.

Respectfully submitted,

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August 5, 2003

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